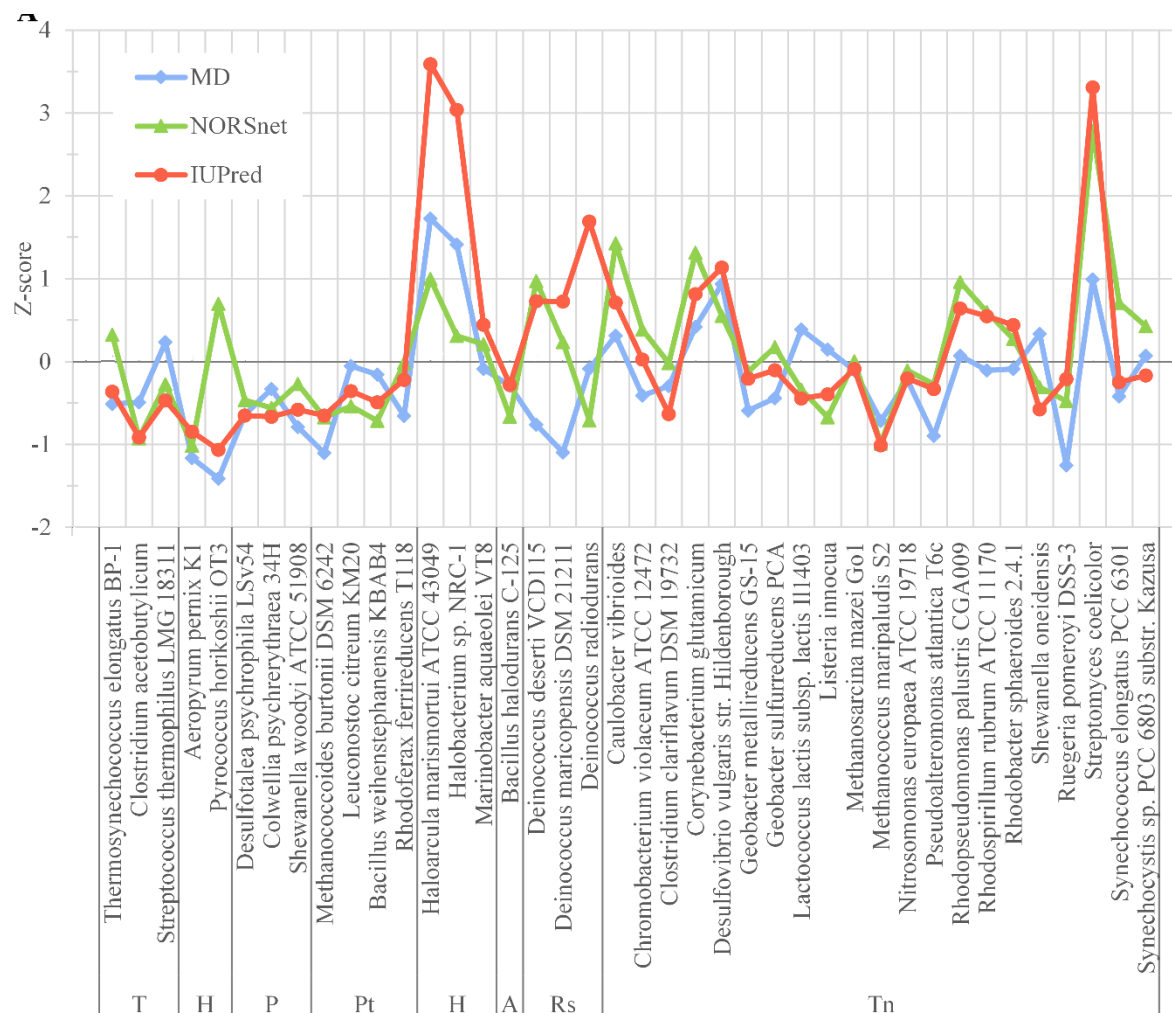


**Fig. S3:**



**Fig. S3: Distribution of disorder content in different organisms for %long30.**

Fractions of proteins with long regions of disorder (here  $\geq 30$  consecutive residues) were predicted by three prediction methods (MD, NORSnet and IUPred). The raw values are standardized using the Z-scores (Eqn. 1) and the mean and standard deviation (sd) obtained from a population of 1613 prokaryotes calculated for each method (positive: higher than the mean; negative: below the mean; integers  $\pm N$  imply  $N \times \text{sd}$  above/below the mean). The taxonomic neighbors section compares the disorder predicted for the closest relatives of the extremophiles. Abbreviations: T, Thermophiles; H, Hyperthermophiles; P, Psychrophiles; Pt, Psychrotolerants; Hal, Halophiles; A, Ahlkalophla; Rs, Radiation resistents; Tn, Taxonomic neighbors.